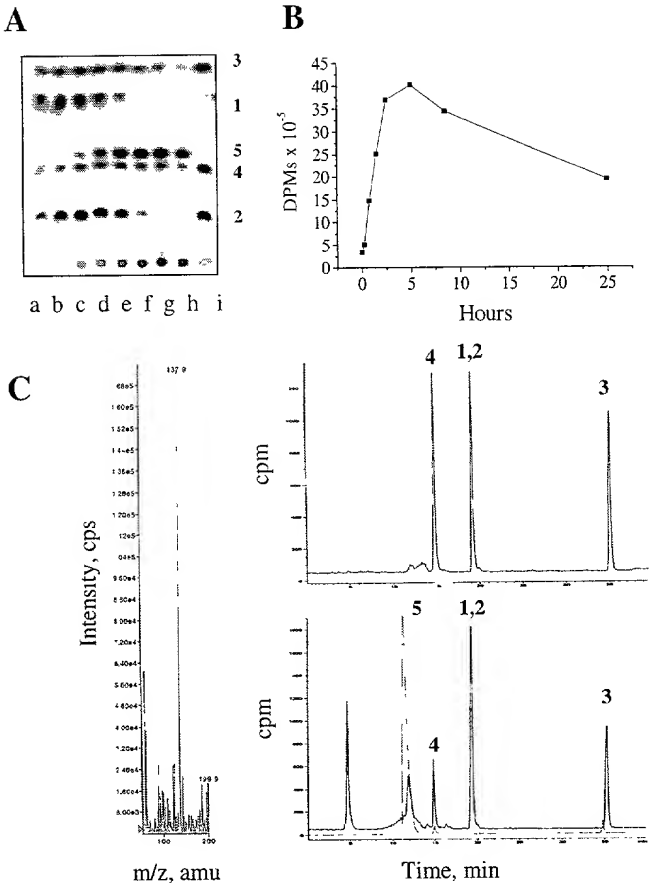

A
3
1
5
4
2
a b c d e f g h i
B
DPMs x 10^-5
45
40
35
30
25
20
15
10
5
0
0 5 10 15 20 25
Hours
C
Intensity, cps
m/z, amu
4 1,2 3
cpm
5 1,2 4 3
cpm
Time, min

FIG. 1

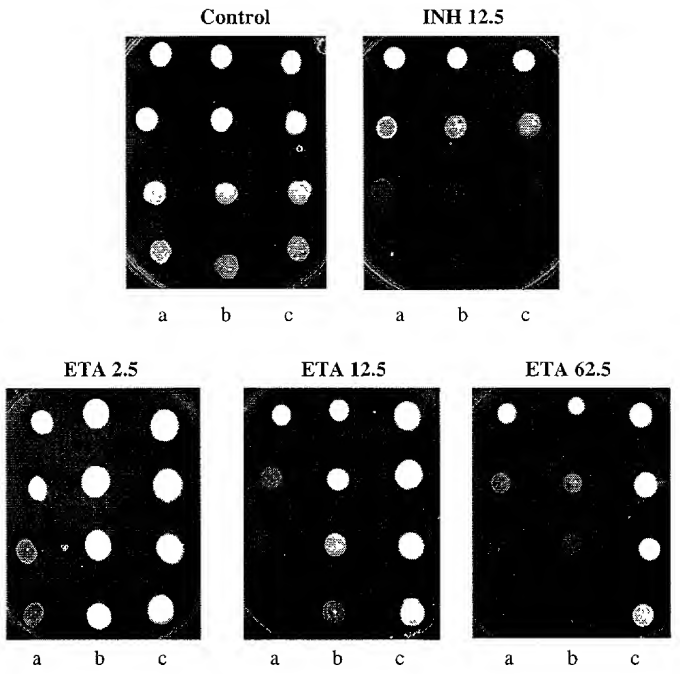


FIG. 2

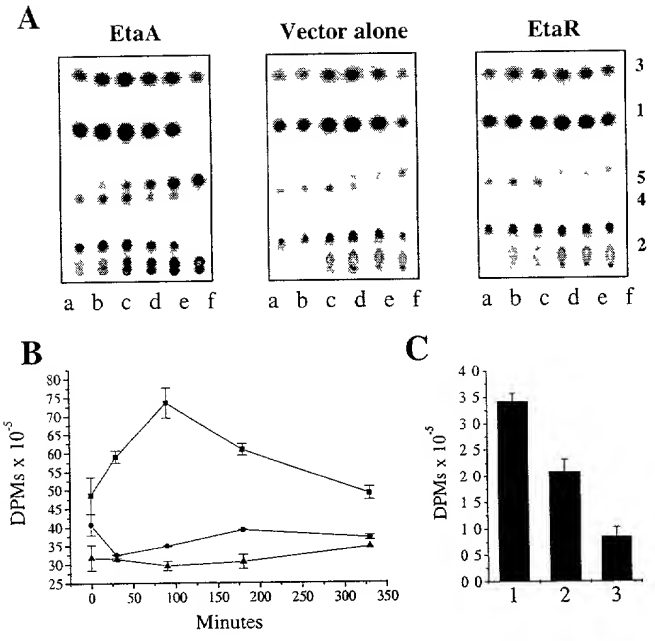
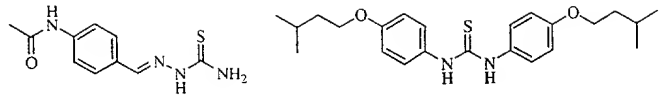

A
EtaA
Vector alone
EtaR
3
1
5
4
2
a b c d e f
a b c d e f
a b c d e f
B
DPMs x 10^-5
80
75
70
65
60
55
50
45
40
35
30
25
0 50 100 150 200 250 300 350
Minutes
C
DPMs x 10^-5
4 0
3 5
3 0
2 5
2 0
1 5
1 0
0 5
0 0
1 2 3

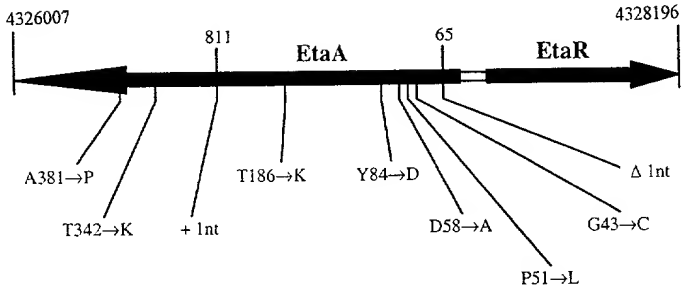
FIG. 3

A



1 2

B



C

Strain	ETA	TA	TC	INH	Nucleotide	Amino-acid
AS1TA$_R$	H	H	H	S	65	-
AS2TA$_R$	H	H/M	M	H	127	G43→C
AS3TA$_R$	L	H	H	H	152	P51→L
AS4TA$_R$	L	L/M	L	M	173	D58→A
AS5TA$_R$	L	H	H	M	250	Y84→D
AS6TA$_R$	L	M	L	M	811	-
AS7TA$_R$	L	L	S	H	1025	T342→K
AS8TA$_R$	L	L	M	M	1025	T342→K
AS9TA$_R$	L	L	M	M	1025	T342→K
AS10TA$_R$	M	H	H	H	1141	A381→P
AS11TA$_R$	H	H	H	S	1141	A381→P
AS12TA$_R$	S	H	H	M	-	-
AS13TA$_R$	S	M	M	S	-	-
AS14TA$_R$	S	S	H	M	-	-
ATCC3580	H	-	-	-	557	T186→K

FIG. 4

SEQ ID No.: 1

EtaA: 1467 bp - M. tuberculosis -

```
                                                        agcgg
        acggtcctcgagaaggttctcggcggtggcgaggatcgc
        cagttcacgatcgtcgccggacggccgcgcggtgcgccg
        gcccctaggcagcgaagcctgactggccgcggaggtggt
        caccctggcagcttactacgtgtcgatagtgtcgacatc
        tcgttgacggcctcgacattacgttgatagcgtggatcc
   1 - atg acc gag cac ctc gac gtt gtc atc gtg
  31 - ggc gct gga atc tcc ggt gtc agc gcg gcc
  61 - tgg cac ctg cag gac cgt tgc ccg acc aag
  91 - agc tac gcc atc ctg gaa aag cgg gaa tcc
 121 - atg ggc ggc acc tgg gat ttg ttc cgt tat
 151 - ccc gga att cgc tcc gac tcc gac atg tac
 181 - acg cta ggt ttc cga ttc cgt ccc tgg acc
 211 - gga cgg cag gcg atc gcc gac ggc aag ccc
 241 - atc ctc gag tac gtc aag agc acc gcg gcc
 271 - atg tat gga atc gac agg cat atc cgg ttc
 301 - cac cac aag gtg atc agt gcc gat tgg tcg
 331 - acc gcg gaa aac cgc tgg acc gtt cac atc
 361 - caa agc cac ggc acg ctc agc gcc ctc acc
 391 - tgc gaa ttc ctc ttt ctg tgc agc ggc tac
 421 - tac aac tac gac gag ggc tac tcg ccg aga
 451 - ttc gcc ggc tcg gag gat ttc gtc ggg ccg
 481 - atc atc cat ccg cag cac tgg ccc gag gac
 511 - ctc gac tac gac gct aag aac atc gtc gtg
 541 - atc ggc agt ggc gca acg gcg gtc acg ctc
 571 - gtg ccg gcg ctg gcg gac tcg ggc gcc aag
 601 - cac gtc acg atg ctg cag cgc tca ccc acc
 631 - tac atc gtg tcg cag cca gac cgg gac ggc
 661 - atc gcc gag aag ctc aac cgc tgg ctg ccg
 691 - gag acc atg gcc tac acc gcg gta cgg tgg
 721 - aag aac gtg ctg cgc cag gcg gcc gtg tac
 751 - agc gcc tgc cag aag tgg cca cgg cgc atg
 781 - cgg aag atg ttc ctg agc ctg atc cag cgc
 811 - cag cta ccc gag ggg tac gac gtg cga aag
 841 - cac ttc ggc ccg cac tac aac ccc tgg gac
 871 - cag cga ttg tgc ttg gtg ccc aac ggc gac
 901 - ctg ttc cgg gcc att cgt cac ggg aag gtc
 931 - gag gtg gtg acc gac acc att gaa cgg ttc
 961 - acc gcg acc gga atc cgg ctg aac tca ggt
 991 - cgc gaa ctg ccg gct gac atc atc att acc
1021 - gca acg ggg ttg aac ctg cag ctt ttt ggt
1051 - ggg gcg acg gcg act atc gac gga caa caa
1081 - gtg gac atc acc acg acg atg gcc tac aag
1111 - ggc atg atg ctt tcc ggc atc ccc aac atg
1141 - gcc tac acg gtt ggc tac acc aat gcc tcc
1171 - tgg acg ctg aag gcc gac ctg gtg tcg gag
1201 - ttt gtc tgt cgc ttg ttg aat tac atg gac
1231 - gac aac ggt ttt gac acc gtg gtc gtc gag
1261 - cga ccg ggc tca gat gtc gaa gag cgg ccc
1291 - ttc atg gag ttc acc cca ggt tac gtg ctg
1321 - cgc tcg ctg gac gag ctg ccc aag cag ggt
1351 - tcg cgt aca ccg tgg cgc ctg aat cag aac
1381 - tac cta cgt gac atc cgg ctc atc cgg cgc
1411 - ggc aag atc gac gac gag ggt ctg cgg ttc
1441 - gcc aaa agg cct gcc ccg gtg ggg gtt
        tagctttagcgacggtttagcgccggtttaggccatagt
        cagacgacgatgatgccgtcgtcgtcgctgtaggcgata
        tcgcccggaacgaatgtcaccccgcccagcgtgatttca
        acgtcgcgttctccggcaccggtcttggtgctcttgcgg
        ggattggtgcccagcgctttgatgccgatgtcgatgccg
        cgcag
```

Figure 5

SEQ ID No.: 2

EtaA: 489 aa - M. tuberculosis -

```
   1 - MTEHLDVVIV GAGISGVSAA WHLQDRCPTK SYAILEKRES MGGTWDLFRY PGIRSDSDMY
  61 - TLGFRFRPWT GRQAIADGKP ILEYVKSTAA MYGIDRHIRF HHKVISADWS TAENRWTVHI
 121 - QSHGTLSALT CEFLFLCSGY YNYDEGYSPR FAGSEDFVGP IIHPQHWPED LDYDAKNIVV
 181 - IGSGATAVTL VPALADSGAK HVTMLQRSPT YIVSQPDRDG IAEKLNRWLP ETMAYTAVRW
 241 - KNVLRQAAVY SACQKWPRRM RKMFLSLIQR QLPEGYDVRK HFGPHYNPWD QRLCLVPNGD
 301 - LFRAIRHGKV EVVTDTIERF TATGIRLNSG RELPADIIIT ATGLNLQLFG GATATIDGQQ
 361 - VDITTTMAYK GMMLSGIPNM AYTVGYTNAS WTLKADLVSE FVCRLLNYMD DNGFDTVVVE
 421 - RPGSDVEERP FMEFTPGYVL RSLDELPKQG SRTPWRLNQN YLRDIRLIRR GKIDDEGLRF
 481 - AKRPAPVGV
```

Figure 6